



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Baumgartner, James W.  
Farrah, Theresa M.  
Foster, Donald C.  
Grant, Frank J.  
O'Hara, Patrick J.

(ii) TITLE OF INVENTION: Testis-Specific Receptor

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.  
(B) STREET: 1201 Eastlake Avenue East  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E.  
(B) REGISTRATION NUMBER: 31,648  
(C) REFERENCE/DOCKET NUMBER: 95-33

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 49..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|           |            |            |           |          |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|------------|------------|-----------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CCCCCCGCC | GGGAGAGAGG | CAATATCAAG | GTTTAAATC | TCGGAGAA | ATG | GCT | TTC |     | 57  |     |     |     |     |     |     |     |
|           |            |            |           |          | Met | Ala | Phe |     |     |     |     |     |     |     |     |     |
|           |            |            |           |          | 1   |     |     |     |     |     |     |     |     |     |     |     |
| GTT       | TGC        | TTG        | GCT       | ATC      | GGA | TGC | TTA | TAT | ACC | TTT | CTG | ATA | AGC | ACA | ACA | 105 |
| Val       | Cys        | Leu        | Ala       | Ile      | Gly | Cys | Leu | Tyr | Thr | Phe | Leu | Ile | Ser | Thr | Thr |     |
| 5         |            |            |           |          |     |     | 10  |     |     |     |     |     | 15  |     |     |     |
| TTT       | GGC        | TGT        | ACT       | TCA      | TCT | TCA | GAC | ACC | GAG | ATA | AAA | GTT | AAC | CCT | CCT | 153 |
| Phe       | Gly        | Cys        | Thr       | Ser      | Ser | Ser | Asp | Thr | Glu | Ile | Lys | Val | Asn | Pro | Pro |     |
| 20        |            |            |           |          |     |     | 25  |     |     |     |     | 30  |     |     | 35  |     |
| CAG       | GAT        | TTT        | GAG       | ATA      | GTG | GAT | CCC | GGA | TAC | TTA | GGT | TAT | CTC | TAT | TTG | 201 |
| Gln       | Asp        | Phe        | Glu       | Ile      | Val | Asp | Pro | Gly | Tyr | Leu | Gly | Tyr | Leu | Tyr | Leu |     |
|           |            |            |           |          |     |     | 40  |     |     |     |     | 45  |     |     | 50  |     |
| CAA       | TGG        | CAA        | CCC       | CCA      | CTG | TCT | CTG | GAT | CAT | TTT | AAG | GAA | TGC | ACA | GTG | 249 |
| Gln       | Trp        | Gln        | Pro       | Pro      | Leu | Ser | Leu | Asp | His | Phe | Lys | Glu | Cys | Thr | Val |     |
|           |            |            |           |          |     |     | 55  |     |     |     |     | 60  |     |     | 65  |     |
| GAA       | TAT        | GAA        | CTA       | AAA      | TAC | CGA | AAC | ATT | GGT | AGT | GAA | ACA | TGG | AAG | ACC | 297 |
| Glu       | Tyr        | Glu        | Leu       | Lys      | Tyr | Arg | Asn | Ile | Gly | Ser | Glu | Thr | Trp | Lys | Thr |     |
|           |            |            |           |          |     |     | 70  |     |     |     |     | 75  |     |     | 80  |     |
| ATC       | ATT        | ACT        | AAG       | AAT      | CTA | CAT | TAC | AAA | GAT | GGG | TTT | GAT | CTT | AAC | AAG | 345 |
| Ile       | Ile        | Thr        | Lys       | Asn      | Leu | His | Tyr | Lys | Asp | Gly | Phe | Asp | Leu | Asn | Lys |     |
|           |            |            |           |          |     |     |     |     |     |     |     | 85  |     |     | 95  |     |

|   |     |
|---|-----|
| GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT<br>Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn<br>100 105 110 115 | 393 |
| GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA<br>Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser<br>120 125 130     | 441 |
| CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT<br>Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr<br>135 140 145     | 489 |
| TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA<br>Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val<br>150 155 160     | 537 |
| CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT<br>Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp<br>165 170 175     | 585 |
| CAT GCA TTA CAG TGT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA<br>His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile<br>180 185 190 195     | 633 |
| GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT<br>Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr<br>200 205 210     | 681 |
| ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT<br>Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr<br>215 220 225     | 729 |
| TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT<br>Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr<br>230 235 240     | 777 |
| CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC<br>Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser<br>245 250 255     | 825 |
| ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG<br>Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu<br>260 265 270 275 | 873 |

|  |     |     |     |      |
|--|-----|-----|-----|------|
| ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA<br>Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu | 280 | 285 | 290 | 921  |
| ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA<br>Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val | 295 | 300 | 305 | 969  |
| GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT<br>Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser | 310 | 315 | 320 | 1017 |
| GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA<br>Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys | 325 | 330 | 335 | 1065 |
| ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT<br>Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val | 340 | 345 | 350 | 1113 |
| ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA<br>Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys | 360 | 365 | 370 | 1161 |
| ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG<br>Met Ile Pro Glu Phe Phe Cys Asp Thr                                   | 375 | 380 |     | 1208 |
| AGACATGGTA TTGACTCAAC AGTTCCAGT CATGGCCAAA TGTTCAATAT GAGTCTCAAT   |     |     |     | 1268 |
| AAACTGAATT TTTCTTGCAG A  |     |     |     | 1289 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val  
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu  
 245 250 255

Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
 260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
 275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu  
 290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly  
 305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu  
 325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu  
 340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr  
 355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GATCCGCC | ATG | GCT | TTC | GTT | TGC | TTG | GCT | ATC | GGA | TGC | TTA | TAT | ACC | 48  |     |
| Met      | Ala | Phe | Val | Cys | Leu | Ala | Ile | Gly | Cys | Leu | Tyr | Thr |     |     |     |
| 1        |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     |
| TTT      | CTG | ATA | AGC | ACA | ACA | TTT | GGC | TGT | ACT | TCA | TCT | TCA | GAC | ACC | 96  |
| Phe      | Leu | Ile | Ser | Thr | Thr | Phe | Gly | Cys | Thr | Ser | Ser | Ser | Asp | Thr |     |
| 15       |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |
| ATA      | AAA | GTT | AAC | CCT | CCT | CAG | GAT | TTT | GAG | ATA | GTG | GAT | CCC | GGA | 144 |
| Ile      | Lys | Val | Asn | Pro | Pro | Gln | Asp | Phe | Glu | Ile | Val | Asp | Pro | Gly |     |
| 30       |     |     |     | 35  |     |     |     |     | 40  |     |     | 45  |     |     |     |
| TTA      | GGT | TAT | CTC | TAT | TTG | CAA | TGG | CAA | CCC | CCA | CTG | TCT | CTG | GAT | 192 |
| Leu      | Gly | Tyr | Leu | Tyr | Leu | Gln | Trp | Gln | Pro | Pro | Leu | Ser | Leu | Asp |     |
| 50       |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |
| TTT      | AAG | GAA | TAC | ACA | GTG | GAA | TAT | GAA | CTA | AAA | TAC | CGA | AAC | ATT | 240 |
| Phe      | Lys | Glu | Tyr | Thr | Val | Glu | Tyr | Glu | Leu | Lys | Tyr | Arg | Asn | Ile |     |
| 65       |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |
| AGT      | GAA | ACA | TGG | AAG | ACC | ATC | ATT | ACT | AAG | AAT | CTA | CAT | TAC | AAA | 288 |
| Ser      | Glu | Thr | Trp | Lys | Thr | Ile | Ile | Thr | Lys | Asn | Leu | His | Tyr | Lys |     |
| 80       |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |
| GGG      | TTT | GAT | CTT | AAC | AAG | GGC | ATT | GAA | GCG | AAG | ATA | CAC | ACG | CTT | 336 |
| Gly      | Phe | Asp | Leu | Asn | Lys | Gly | Ile | Glu | Ala | Lys | Ile | His | Thr | Leu |     |
| 95       |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |
| CCA      | TGG | CAA | TGC | ACA | AAT | GGA | TCA | GAA | GTT | CAA | AGT | TCC | TGG | GCA | 384 |
| Pro      | Trp | Gln | Cys | Thr | Asn | Gly | Ser | Glu | Val | Gln | Ser | Ser | Trp | Ala |     |
| 110      |     |     |     | 115 |     |     |     |     | 120 |     |     | 125 |     |     |     |
| ACT      | ACT | TAT | TGG | ATA | TCA | CCA | GGA | ATT | CCA | GAA | ACT | AAA | GTT | CAG | 432 |
| Thr      | Thr | Tyr | Trp | Ile | Ser | Pro | Gln | Gly | Ile | Pro | Glu | Thr | Lys | Val |     |
| 130      |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |     |
| GAT      | ATG | GAT | TGC | GTA | TAT | TAC | AAT | TGG | CAA | TAT | TTA | CTC | TGT | TCT | 480 |
| Asp      | Met | Asp | Cys | Val | Tyr | Tyr | Asn | Trp | Gln | Tyr | Leu | Leu | Cys | Ser |     |
| 145      |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |
| AAA      | CCT | GGC | ATA | GGT | GTA | CTT | GAT | ACC | AAT | TAC | AAC | TTG | TTT | TAC | 528 |
| Lys      | Pro | Gly | Ile | Gly | Val | Leu | Leu | Asp | Thr | Asn | Tyr | Asn | Leu | Phe |     |
| 160      |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

|   |      |
|---|------|
| TGG TAT GAG GGC TTG GAT CTT GCA TTA CAG TGT GTT GAT TAC ATC AAG<br>Trp Tyr Glu Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys<br>175                   180                   185                       | 576  |
| GCT GAT GGA CAA AAT ATA GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA<br>Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser<br>190                   195                   200                   205 | 624  |
| GAC TAT AAA GAT TTC TAT ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG<br>Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys<br>210                   215                   220                       | 672  |
| CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA<br>Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys<br>225                   230                   235                       | 720  |
| CCT TTG CCG CCA GTC TAT CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA<br>Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu<br>240                   245                   250                       | 768  |
| ATT AAG CTG AAA TGG GGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT<br>Ile Lys Leu Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys<br>255                   260                   265                       | 816  |
| TTT GAT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT<br>Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr<br>270                   275                   280                   285 | 864  |
| GCT ACA GTT GAA AAT GAA ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC<br>Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr<br>290                   295                   300                       | 912  |
| CGA CAA TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA<br>Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser<br>305                   310                   315                       | 960  |
| GAT GAC GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT<br>Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly<br>320                   325                   330                       | 1008 |
| GAA GAC CTA TCG AAG AAA ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT<br>Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly<br>335                   340                   345                       | 1056 |

TTC ATC TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG 1104  
 Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys  
 350 355 360 365

CCA AAC ACC TAC CCA AAA ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT  
 1159

Pro Asn Thr Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr  
 370 375 380

CCTCTAGA 1167

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
 1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val  
 20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
 35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
 50 55 60

Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
 65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
 85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
 100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
 115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
 130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
 145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
 165 170 175

Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
 180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
 195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
 210 215 220

Ser Ser Tyr Phe Thr Phē Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
 225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu  
 245 250 255

Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
 260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
 275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu  
 290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly  
 305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu  
 325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu  
 340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr  
 355                           360                           365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr  
 370                           375                           380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Trp Ser Xaa Trp Ser  
 1                         5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..1126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTTGGAGAA ATG GCT TTC GTC TAC TTG GCT ATC AGA TGC TTA TGT ACC  
 Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr  
 1                         5                           10

|  |     |     |     |     |
|--|-----|-----|-----|-----|
| TTT CTG ATA AGC ACA ACA TTC GGC TAT ACT TCA ACT TCA GAC ACC GAG<br>Phe Leu Ile Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu | 15  | 20  | 25  | 97  |
| ATA AAA GTT AAC CCA CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAT<br>Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr | 30  | 35  | 40  | 145 |
| TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT AAT<br>Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn | 50  | 55  | 60  | 193 |
| TTT AAG GAA TGC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT<br>Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly | 65  | 70  | 75  | 241 |
| AGT GAA ACA TGG ACG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT<br>Ser Glu Thr Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp | 80  | 85  | 90  | 289 |
| GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACA CTT TTA<br>Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu | 95  | 100 | 105 | 337 |
| CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA<br>Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu | 110 | 115 | 120 | 385 |
| GCT ACT TAT TGG ATA TCG CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG<br>Ala Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln | 130 | 135 | 140 | 433 |
| GAT ATG GAT TGT GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG<br>Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp | 145 | 150 | 155 | 481 |
| AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC<br>Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr | 160 | 165 | 170 | 529 |
| TGG TAT GAG GGC TTG GAT CGT GCA TTA CAG TGT GTT GAT TAC ATC AAG<br>Trp Tyr Glu Gly Leu Asp Arg Ala Leu Gln Cys Val Asp Tyr Ile Lys | 175 | 180 | 185 | 577 |

|   |      |
|---|------|
| GTT GAT GGA CAA AAT ATT GGA TGC AGA TTT CCC TAT TTG GAG TCA TCA<br>Val Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser<br>190 195 200 205 | 625  |
| GAC TAT AAA GAT TTC TAC ATT TGT GTT AAT GGA TCA TCA GAA ACC AAG<br>Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys<br>210 215 220     | 673  |
| CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA<br>Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys<br>225 230 235     | 721  |
| CCT TTG CCA CCA GTC TGT CTT ACT TGT ACT CAG GAG AGT TTA TAT GAA<br>Pro Leu Pro Pro Val Cys Leu Thr Cys Thr Gln Glu Ser Leu Tyr Glu<br>240 245 250     | 769  |
| ATT AAG CTG AAA TGG AGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT<br>Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys<br>255 260 265     | 817  |
| TTT GTT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT<br>Phe Val Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr<br>270 275 280 285 | 865  |
| ACC ACA GTT GAA AAT GAA ACG TAC ACC TTG AAA ATA ACA AAT GAA ACC<br>Thr Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr<br>290 295 300     | 913  |
| CGA CAG TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA<br>Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser<br>305 310 315     | 961  |
| GAT GAT GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGT TGG GAA GTT<br>Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Val<br>320 325 330     | 1009 |
| GAA GAA CTA TTG AAG AAA ACT TTG CTA CTT TTC TTG TTA CCA TTT GGT<br>Glu Glu Leu Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly<br>335 340 345     | 1057 |
| TTC ATA TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG TGT AAG<br>Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys<br>350 355 360 365 | 1105 |
| AGA GAC AGC TAC CCG AAA ATG   | 1126 |

Arg Asp Ser Tyr Pro Lys Met  
370

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr Phe Leu Ile  
1 5 10 15

Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu Ile Lys Val  
 20                    25                    30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn Phe Lys Glu  
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80

Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Ala Thr Tyr  
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
 165 170 175

Gly Leu Asp Arg Ala Leu Gln Cys Val Asp Tyr Ile Lys Val Asp Gly  
 180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys  
 195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys Pro Ile Arg  
 210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
 225 230 235 240

Pro Val Cys Leu Thr Cys Thr Gln Glu Ser Leu Tyr Glu Ile Lys Leu  
 245 250 255

Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Val Tyr  
 260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Thr Thr Val  
 275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr Arg Gln Leu  
 290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly  
 305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Val Glu Glu Leu  
 325 330 335

Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly Phe Ile Leu  
 340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys Arg Asp Ser  
 355 360 365

Tyr Pro Lys Met  
 370

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGGTCCTTCC CATGTTTCAC TACCA

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCGGTATT TTAGTTCATA TTCCA

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGAATTTGG AGTGAGTGGA GTGAT

25

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9937

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAGACCTA TCGAAGAAAA CTTTG

25

## (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9800

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGCTTCG TTTGCTTGGC TATCG

25

## (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTTGATAT GGAAAGTCTT CATGTATC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: AP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCATCCTAAC TACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: AP2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCTGATAGGC TTGTTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATAGCCAAGC AAACGAAAGC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCTGGCATA GGTGTACTTC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTGCCGCCAG TCTATCTTAC

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGGGGTCTA GAGGAAAGTC TTCATGTATC ACAG

34

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG10319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGGGGCTGG AGCTCGGAGA AATGGCTTTC GTT

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCCCCACTG TCTCTGGATC ATTTT

25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACCTTCCCA GCATTGTTA TCACT

25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG10320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGGGGAGAT CTTCAGACAC CGAGATAAAA GTT

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG10318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGGGGGCTCG AGTTTCTTCG ATAGGTCTTC ACC

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTACTCTGTT CTTGGAAACC TGG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG10082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACTCTGTTCT TGGAAACCTG G

21

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi.i) IMMEDIATE SOURCE:

- (B) CLONE: ZG10083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAATGAAACA TACACCTTGA AAAC

24

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCATTGTTA TCACTCCACT C

21

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTCACTTTGC TTCTTACTAC AAA

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACTAGCAGA TCTGGGCTCT TTCTTCGATA GGTCTTCAC

39

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG10314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCGTGATTCT CTGGTCGGTG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG10315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGATTGCTT TGGCGGTGAG

20